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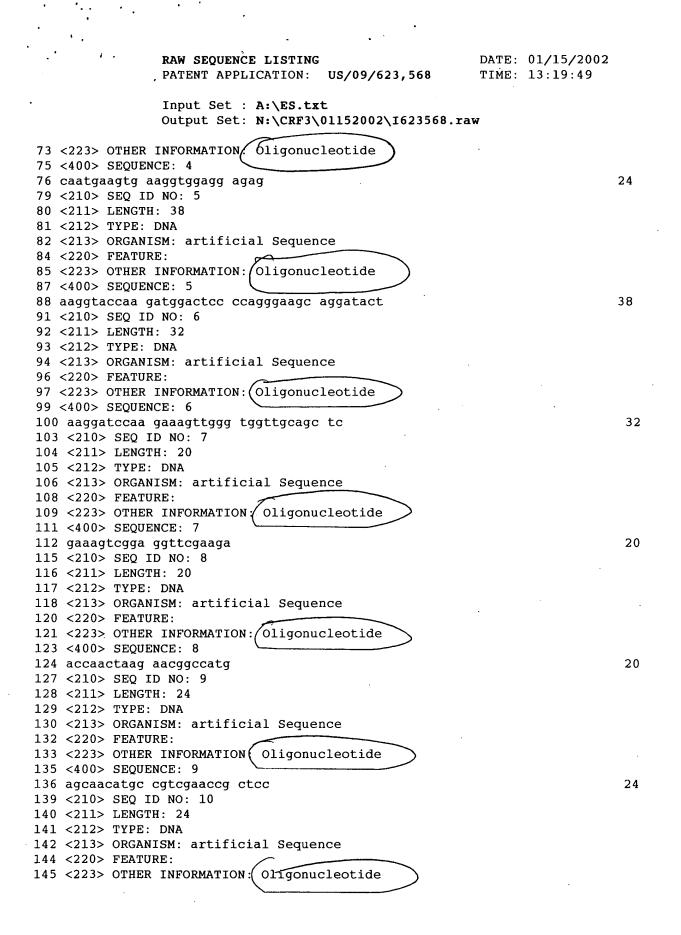
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	, ,	Raw Sequence Listing Error Summary
	ERROR DETECTED	SUCCESTED CORRECTION SERIAL NUMBER: 09/623,568
<u>.</u>	ATTN: NEW RULES CASES	S: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOF
	1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
•	2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
	3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
·	4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
	SVariable Length	Sequence(s)contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
APR 0 8 2002 TECH CENTER 1600/2900	6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
	57Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading). (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
		Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
	8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
	9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220> <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
	10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
	11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
	12PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
	13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.
	 	AMC/MH - Biotechnology Systems Branch - 08/21/2001
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DATE: 01/15/2002 RAW SEQUENCE LISTING TIME: 13:19:49 PATENT APPLICATION: US/09/623,568 pp 1-2 Input Set : A:\ES.txt Output Set: N:\CRF3\01152002\1623568.raw **Does Not Comply** 3 <110> APPLICANT: Miller, Barbara Corrected Diskette Needed Osmani, Stephen 4 5 Clawson, Gary 6 Zhang, Min-Ying 7 Norris, James 9 <120> TITLE OF INVENTION: Use of Human Homolog Of A Nuclear Migration Gene For Treatment And 10 Diagnosis Of Cancer 12 <130> FILE REFERENCE: PSU-0016 14 <140> CURRENT APPLICATION NUMBER: 09/623,568 15 <141> CURRENT FILING DATE: 2001-03-23 17 <150> PRIOR APPLICATION NUMBER: 60/076,885 18 <151> PRIOR FILING DATE: 1998-03-05 20 <150> PRIOR APPLICATION NUMBER: PCT US99/04996 21 <151> PRIOR FILING DATE: 1999-03-05 23 <160> NUMBER OF SEQ ID NOS: 16 25 <170> SOFTWARE: PatentIn version 3.1 27 <210> SEQ ID NO: 1 28 <211> LENGTH: 14 29 <212> TYPE: PRT 30 <213> ORGANISM; artificial Sequence insufficient explanation - give source of In Asp Gln Arg Gln Lys genetic material (see item 11 on Erron Summary fheet) 32 <220> FEATURE: 33 <223> OTHER INFORMATION: Peptide 35 <400> SEQUENCE: 1 37 Gly Cys Met Val Glu Lys Met Met Tyr Asp Gln Arg Gln Lys 38 1 41 <210> SEQ ID NO: 2 42 <211> LENGTH: 15 43 <212> TYPE: PRT 44 <213> ORGANISM: artificial Sequence 46 <220> FEATURE: same and 47 <223> OTHER INFORMATION: (Peptide 49 <400> SEQUENCE: 2 51 Asn Gly Ser Leu Asp Ser Pro Gly Lys Gln Asp Thr Glu Glu Asp 10 15 52 1 5 55 <210> SEQ ID NO: 3 56 <211> LENGTH: 24 57 <212> TYPE: DNA 58 <213> ORGANISM: artificial Sequence same type) enn 60 <220> FEATURE: 61 <223> OTHER INFORMATION: (Oligonucleotide 63 <400> SEQUENCE: 3 24 64 ttctgttcgt ctgaagttgg cagc 67 <210> SEQ ID NO: 4 68 <211> LENGTH: 24 69 <212> TYPE: DNA 70 <213> ORGANISM: artificial Sequence 72 <220> FEATURE:



DATE: 01/15/2002 RAW SEQUENCE LISTING TIME: 13:19:49 PATENT APPLICATION: US/09/623,568 Input Set : A:\ES.txt Output Set: N:\CRF3\01152002\1623568.raw 147 <400> SEQUENCE: 10 24 148 ggagcggttc gacggcatgt tgct 151 <210> SEQ ID NO: 11 152 <211> LENGTH: 1281 153 <212> TYPE: DNA 154 <213> ORGANISM: Homo sapiens 156 <400> SEQUENCE: 11 60 157 ctagagtgca gagctccggg acgtggatcg gagccggcgc gatgggcgga gagcaggagg 159 aggagcggtt cgacggcatg ttgctggcca tggctcagca gcacgagggc ggcgtgcagg 120 180 161 agettgtgaa cacettette agetteette gaegeaaaae agaetttte attggaggag 163 aaqaaqqqat ggcagagaag cttatcacac agactttcag ccaccacaat cagctggcac 240 165 aqaaqacccq gcqggagaag agagcccggc aggaggccga gcggcgggag aaggcggagc 300 167 gggcggccag actggccaag gaagccaagt cagagacete agggeeeeag atcaaggage 360 169 taactgatga agaggcagag aggctgcagc tagagattga ccagaaaaag gatgcagaga 420 171 atcatgagge ccageteaag aacggeagee ttgacteece agggaageag gatactgagg 480 540 173 aagatgagga ggaagatgag aaggacaaag gaaaactgaa gcccaaccta ggcaacgggg 600 175 cagacctgcc caattaccgc tggacccaga ccctgtcgga gctggacctg gcggtccctt 177 tctgtgtgaa cttccggctg aaagggaagg acatggtggt ggacatccag cggcggcacc 660 179 tccgggtggg gctcaagggg cagccagcga tcattgatgg ggagctctac aatgaagtga 720 780 181 aggtggagga gagctcgtgg ctcattgagg acggcaaggt ggtgactgtg catctggaga 183 agatcaataa gatggagtgg tggagccgct tggtgtccag tgaccctgag atcaacacca 840 900 185 agaagattaa ccctgagaat tccaagctgt cagacctgga cagtgagact cgcagcatgg 960 187 tggaaaagat gatgtatgac cagcgacaga agtccatggg gctgccaact tcagacgaac 1020 189 agaagaaaca ggagattetg aagaagttea tggateaaca teeggagatg gatttteea 191 aggctaaatt caactagccc ctgttttttc ctccctgaac tcttggggct gagctgcaac 1080 193 cacccaactt totttoccac tottototgg gaottgtggg cotcagggot tggggcaggc 1140 195 atgggactgg cccaggcaca caggtcccgg ggcatcagga gaaaggctgg gtcttgggac 1200 197 cttgtcctcc ccagttggcc tactgttaca cattaaaacg atttgcccag ctcaaaaaaa 1260 199 aaaaaaaaaa aaaaaaaaaa a 1281 202 <210> SEQ ID NO: 12 203 <211> LENGTH: 331 204 <212> TYPE: PRT 205 <213> ORGANISM: Homo sapiens 207 <400> SEQUENCE: 12 209 Met Gly Gly Glu Gln Glu Glu Glu Arg Phe Asp Gly Met Leu Leu Ala 10 15 210 1 5 213 Met Ala Gln Gln His Glu Gly Gly Val Gln Glu Leu Val Asn Thr Phe 25 214 20 30 217 Phe Ser Phe Leu Arg Arg Lys Thr Asp Phe Phe Ile Gly Gly Glu Glu 45 218 40 35 221 Gly Met Ala Glu Lys Leu Ile Thr Gln Thr Phe Ser His His Asn Gln 222 50 55 225 Leu Ala Gln Lys Thr Arg Arg Glu Lys Arg Ala Arg Gln Glu Ala Glu 80 226 65 70 75 229 Arg Arg Glu Lys Ala Glu Arg Ala Ala Arg Leu Ala Lys Glu Ala Lys 230 85 90 95 233 Ser Glu Thr Ser Gly Pro Gln Ile Lys Glu Leu Thr Asp Glu Glu Ala 105 110 234 100

237 Glu Arg Leu Gln Leu Glu Ile Asp Gln Lys Lys Asp Ala Glu Asn His

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DATE: 01/15/2002 TIME: 13:19:49

Input Set : A:\ES.txt
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241 Glu Ala Gln Leu Lys Asn Gly Ser Leu Asp Ser Pro Gly Lys Gln Asp 245 Thr Glu Glu Asp Glu Glu Glu Asp Glu Lys Asp Lys Gly Lys Leu Lys 246 145 249 Pro Asn Leu Gly Asn Gly Ala Asp Leu Pro Asn Tyr Arg Trp Thr Gln 253 Thr Leu Ser Glu Leu Asp Leu Ala Val Pro Phe Cys Val Asn Phe Arg . 257 Leu Lys Gly Lys Asp Val Val Val Asp Ile Gln Arg Arg His Leu Arg 261 Val Gly Leu Lys Gly Gln Pro Ala Ile Ile Asp Gly Glu Leu Tyr Asn . 265 Glu Val Lys Val Glu Glu Ser Ser Trp Leu Ile Glu Asp Gly Lys Val 266 225 269 Val Thr Val His Leu Glu Lys Ile Asn Lys Met Glu Trp Trp Ser Arg 273 Leu Val Ser Ser Asp Pro Glu Ile Asn Thr Lys Lys Ile Asn Pro Glu 277 Asn Ser Lys Leu Ser Asp Leu Asp Ser Glu Thr Glu Ser Met Val Glu 278 275 281 Lys Met Met Tyr Asp Gln Arg Gln Lys Ser Met Gly Leu Pro Thr Ser 285 Asp Glu Gln Lys Lys Gln Glu Ile Leu Lys Lys Phe Met Asp Gln His 286 305 289 Pro Glu Met Asp Phe Ser Lys Ala Lys Phe Asn 293 <210> SEQ ID NO: 13 294 <211> LENGTH: 332 295 <212> TYPE: PRT 296 <213> ORGANISM: Rattus rattus 298 <400> SEQUENCE: 13 300 Met Gly Gly Glu Gln Glu Glu Glu Arg Phe Asp Gly Met Leu Leu Ala 301 1 304 Met Ala Gln Gln His Glu Gly Gly Val Gln Glu Leu Val Asn Thr Phe 308 Phe Ser Phe Leu Arg Arg Lys Thr Asp Phe Phe Ile Gly Gly Glu Glu 312 Gly Met Ala Glu Lys Leu Ile Thr Gln Thr Phe Asn His His Asn Gln 316 Leu Ala Gln Lys Ala Arg Arg Glu Lys Arg Ala Arg Gln Leu Thr Glu 317 65 320 Arg Arg Glu Lys Ala Glu Arg Ala Ala Arg Leu Ala Lys Glu Ala Lys 324 Ala Glu Thr Pro Gly Pro Gln Ile Lys Glu Leu Thr Asp Leu Lys Ala 328 Glu Arg Leu Gln Leu Glu Ile Asp Gln Lys Lys Asp Ala Glu Asn His 332 Glu Val Gln Leu Lys Asn Gly Ser Leu Asp Ser Pro Gly Lys Gln Asp

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Input Set : A:\ES.txt
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336 Ala Leu Leu Glu Glu Asp Glu Glu Asp Glu Lys Asp Lys Gly Lys Leu 337 145 340 Lys Pro Asn Leu Gly Asn Gly Ala Asp Leu Pro Asn Tyr Arg Trp Thr 344 Gln Thr Leu Ser Phe Leu Asp Leu Ala Val Pro Phe Arg Val Ser Phe 348 Arg Leu Lys Gly Lys Gln Val Val Val Asp Ile Gln Arg Arg His Leu 352 Arg Val Gly Leu Lys Gly Gln Ala Pro Val Ile Asp Gly Glu Leu Tyr • 356 Asn Glu Val Lys Val Glu Glu Ser Ser Trp Leu Ile Glu Asp Gly Lys 357 225 360 Val Val Thr Val His Leu Glu Lys Ile Asn Lys Met Glu Trp Trp Asn 364 Arg Leu Val Thr Ser Asp Pro Glu Ile Asn Thr Lys Lys Ile Asn Pro 368 Glu Asn Ser Lys Leu Ser Asp Leu Asp Ser Glu Thr Arg Ser Met Val 372 Glu Lys Met Met Tyr Asp Gln Àrg Gln Lys Ser Met Gly Leu Pro Thr 376 Ser Asp Glu Gln Lys Lys Gln Glu Ile Leu Lys Lys Phe Met Asp Gln 377 305 380 His Pro Glu Met Asp Phe Ser Lys Ala Lys Phe Asn 384 <210> SEQ ID NO: 14 385 <211> LENGTH: 202 386 <212> TYPE: PRT 387 <213> ORGANISM: Aspergillus nidulans 389 <400> SEQUENCE: 14 391 Met Ser Glu Gln Glu Pro Ser Ser Ala Asp Leu Ala Ala Arg Glu Ala 392 1 395 Glu Glu Lys Gln Arg Lys Ala Ala Glu Glu Ala Glu Gln Ala Thr Leu 399 Pro Tyr Lys Asn Thr Gln Thr Ile Arg Asp Val Asp Val Phe Thr Thr 403 Ile Pro Val Ser Ala Asn Leu Lys Gly Arg Asp Leu Asp Val Val Leu 407 Lys Lys Asp Ser Ile Lys Val Lys Val Lys Gly Glu Asn Gly Glu Val 408 65 411 Phe Ile Asp Gly Gln Phe Pro His Pro Ile Lys Pro Ser Glu Ser Ser 415 Trp Thr Leu Glu Thr Thr Ser Lys Pro Pro Phe Thr Gly Lys Glu Val 419 Ser Ile His Leu Asp Lys Val Asn Gln Met Glu Trp Trp Ala Met Val 423 Val Thr Thr Ala Pro Lys Ile Asp Val Ser Lys Ile Thr Phe Glu Asn 427 Ser Ser Leu Ser Asp Leu Asp Gly Glu Thr Arg Ala Met Val Glu Lys

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

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VERIFICATION SUMMARY • PATENT APPLICATION: US/09/623,568

DATE: 01/15/2002 TIME: 13:19:50

Input Set : A:\ES.txt
Output Set: N:\CRF3\01152002\I623568.raw

.L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16